```
AATTCGTTCT ACCTTCTCTG AACCCCAGTG GTGTGTCAAG GCCGGACTGG GAGCTTGGGG   60

GAAGAGGAAG AGGAAGAGGA ATCTGCGGCT CATCCAGGGA TCAGGGTCCT TCCCAAGTGG  120

CCACTCAGAG GGGACTCAGA GCAAGTCTAG ATTTGTGTGG CAGAGAGAGA CAGCTCTCGT  180

TTGGCCTTGG GGAGGCACAA GTCTGTTGAT AACCTGAAGA CA                      222

ATG GAT GTC GAT GAG GGT CAA GAC ATG TCC CAA GTT TCA GGA AAG GAG      270
Met Asp Val Asp Glu Gly Gln Asp Met Ser Gln Val Ser Gly Lys Glu
1               5                  10                  15

AGC CCC CCA GTC AGT GAC ACT CCA GAT GAA GGG GAT GAG CCC ATG CCT      318
Ser Pro Pro Val Ser Asp Thr Pro Asp Glu Gly Asp Glu Pro Met Pro
            20                  25                  30

GTC CCT GAG GAC CTG TCC ACT ACC TCT GGA GCA CAG CAG AAC TCC AAG      366
Val Pro Glu Asp Leu Ser Thr Thr Ser Gly Ala Gln Gln Asn Ser Lys
        35                  40                  45

AGT GAT CGA GGC ATG GGT GAA CGG CCT TTC CAG TGC AAC CAG TCT GGG      414
Ser Asp Arg Gly Met Gly Gln Arg Pro Phe Gln Cys Asn Gln Ser Gly
    50                  55                  60

GCC TCC TTT ACC CAG AAA GGC AAC CTC CTG CGG CAC ATC AAG CTG CAC      462
Ala Ser Phe Thr Gln Lys Gly Asn Leu Leu Arg His Ile Lys Leu His
65                  70                  75                  80

TCG GGT GAG AAG CCC TTC AAA TGC CAT CTT TGC AAC TAT GCC TGC CGC      510
Ser Gly Glu Lys Pro Phe Lys Cys His Leu Cys Asn Tyr Ala Cys Arg
                85                  90                  95

CGG AGG GAC GCC CTC ACC GGC CAC CTG AGG ACG CAC TCC GTT GGT AAG      558
Arg Arg Asp Ala Leu Thr Gly His Leu Arg Thr His Ser Val Gly Lys
            100                 105                 110

CCT CAC AAA TGT GGA TAT TGT GGC CGG AGC TAT AAA CAG CGA AGC TCT      606
Pro His Lys Cys Gly Tyr Cys Gly Arg Ser Tyr Lys Gln Arg Ser Ser
        115                 120                 125

TTA GAG GAG CAT AAA GAG CGA TGC CAC AAC TAC TTG GAA AGC ATG GGC      654
Leu Glu Glu His Lys Glu Arg Cys His Asn Tyr Leu Glu Ser Met Gly
    130                 135                 140

CTT CCG GGC GTG TGC CCA GTC ATT AAG GAA GAA ACT AAC CAC AAC GAG      702
Leu Pro Gly Val Cys Pro Val Ile Lys Glu Glu Thr Asn His Asn Glu
145                 150                 155                 160

ATG GCA GAA GAC CTG TGC AAG ATA GGA GCA GAG AGG TCC CTT GTC CTG      750
Met Ala Glu Asp Leu Cys Lys Ile Gly Ala Glu Arg Ser Leu Val Leu
                165                 170                 175

GAC AGG CTG GCA AGC AAT GTC GCC AAA CGT AAG AGC TCT ATG CCT CAG      798
Asp Arg Leu Ala Ser Asn Val Ala Lys Arg Lys Ser Ser Met Pro Gln
            180                 185                 190
```

FIG. 1A

```
AAA TTT CTT GGA GAC AAG TGC CTG TCA GAC ATG CCC TAT GAC AGT GCC    846
Lys Phe Leu Gly Asp Lys Cys Leu Ser Asp Met Pro Tyr Asp Ser Ala
        195                 200                 205

AAC TAT GAG AAG GAG GAT ATG ATG ACA TCC CAC GTG ATG GAC CAG GCC    894
Asn Tyr Glu Lys Glu Asp Met Met Thr Ser His Val Met Asp Gln Ala
    210                 215                 220

ATC AAC AAT GCC ATC AAC TAC CTG GGG GCT GAG TCC CTG CGC CCA TTG    942
Ile Asn Asn Ala Ile Asn Tyr Leu Gly Ala Glu Ser Leu Arg Pro Leu
225                 230                 235                 240

GTG CAG ACA CCC CCC GGT AGC TCC GAG GTG GTG CCA GTC ATC AGC TCC    990
Val Gln Thr Pro Pro Gly Ser Ser Glu Val Val Pro Val Ile Ser Ser
                245                 250                 255

ATG TAC CAG CTG CAC AAG CCC CCC TCA GAT GGC CCC CCA CGG TCC AAC   1038
Met Tyr Gln Leu His Lys Pro Pro Ser Asp Gly Pro Pro Arg Ser Asn
            260                 265                 270

CAT TCA GCA CAG GAC GCC GTG GAT AAC TTG CTG CTG CTG TCC AAG GCC   1086
His Ser Ala Gln Asp Ala Val Asp Asn Leu Leu Leu Leu Ser Lys Ala
        275                 280                 285

AAG TCT GTG TCA TCG GAG CGA GAG GCC TCC CCG AGC AAC AGC TGC CAA   1134
Lys Ser Val Ser Ser Glu Arg Glu Ala Ser Pro Ser Asn Ser Cys Gln
    290                 295                 300

GAC TCC ACA GAT ACA GAG AGC AAC GCG GAG GAA CAG CGC AGC GGC CTT   1182
Asp Ser Thr Asp Thr Glu Ser Asn Ala Glu Glu Gln Arg Ser Gly Leu
305                 310                 315                 320

ATC TAC CTA ACC AAC CAC ATC AAC CCG CAT GCA CGC AAT GGG CTG GCT   1230
Ile Tyr Leu Thr Asn His Ile Asn Pro His Ala Arg Asn Gly Leu Ala
                325                 330                 335

CTC AAG GAG GAG CAG CGC GCC TAC GAG GTG CTG AGG GCG GCC TCA GAG   1278
Leu Lys Glu Glu Gln Arg Ala Tyr Glu Val Leu Arg Ala Ala Ser Glu
            340                 345                 350

AAC TCG CAG GAT GCC TTC CGT GTG GTC AGC ACG AGT GGC GAG CAG CTG   1326
Asn Ser Gln Asp Ala Phe Arg Val Val Ser Thr Ser Gly Glu Gln Leu
        355                 360                 365

AAG GTG TAC AAG TGC GAA CAC TGC CGC GTG CTC TTC CTG GAT CAC GTC   1374
Lys Val Tyr Lys Cys Glu His Cys Arg Val Leu Phe Leu Asp His Val
    370                 375                 380

ATG TAT ACC ATT CAC ATG GGC TGC CAT GGC TGC CAT GGC TTT CGG GAT   1422
Met Tyr Thr Ile His Met Gly Cys His Gly Cys His Gly Phe Arg Asp
385                 390                 395                 400

CCC TTT GAG TGT AAC ATG TGT GGT TAT CAC AGC CAG GAC AGG TAC GAG   1470
Pro Phe Glu Cys Asn Met Cys Gly Tyr His Ser Gln Asp Arg Tyr Glu
                405                 410                 415
```

FIG. 1B

```
TTC TCA TCC CAT ATC ACG CGG GGG GAG CAT CGT TAC CAC CTG AGC        1515
Phe Ser Ser His Ile Thr Arg Gly Glu His Arg Tyr His Leu Ser
            420                 425                 430

TAAACCCAGC CAGGCCCCAC TGAAGCACAA AGATAGCTGG TTATGCCTCC TTCCCGGCAG  1575

CTGGACCCAC AGCGGACAAT GTGGGAGTGG ATTTGCAGGC AGCATTTGTT CTTTTATGTT  1635

GGTTGTTTGG CGTTTCATTT GCGTTGGAAG ATAAGTTTTT AATGTTAGTG ACAGGATTGC  1695

ATTGCATCAG CAACATTCAC AACATCCATC CTTCTAGCCA GTTTTGTTCA CTGGTAGCTG  1755

AGGTTTCCCG GATATGTGGC TTCCTAACAC TCT                               1788
```

(SEQ.ID.NO:1)

FIG. 1C

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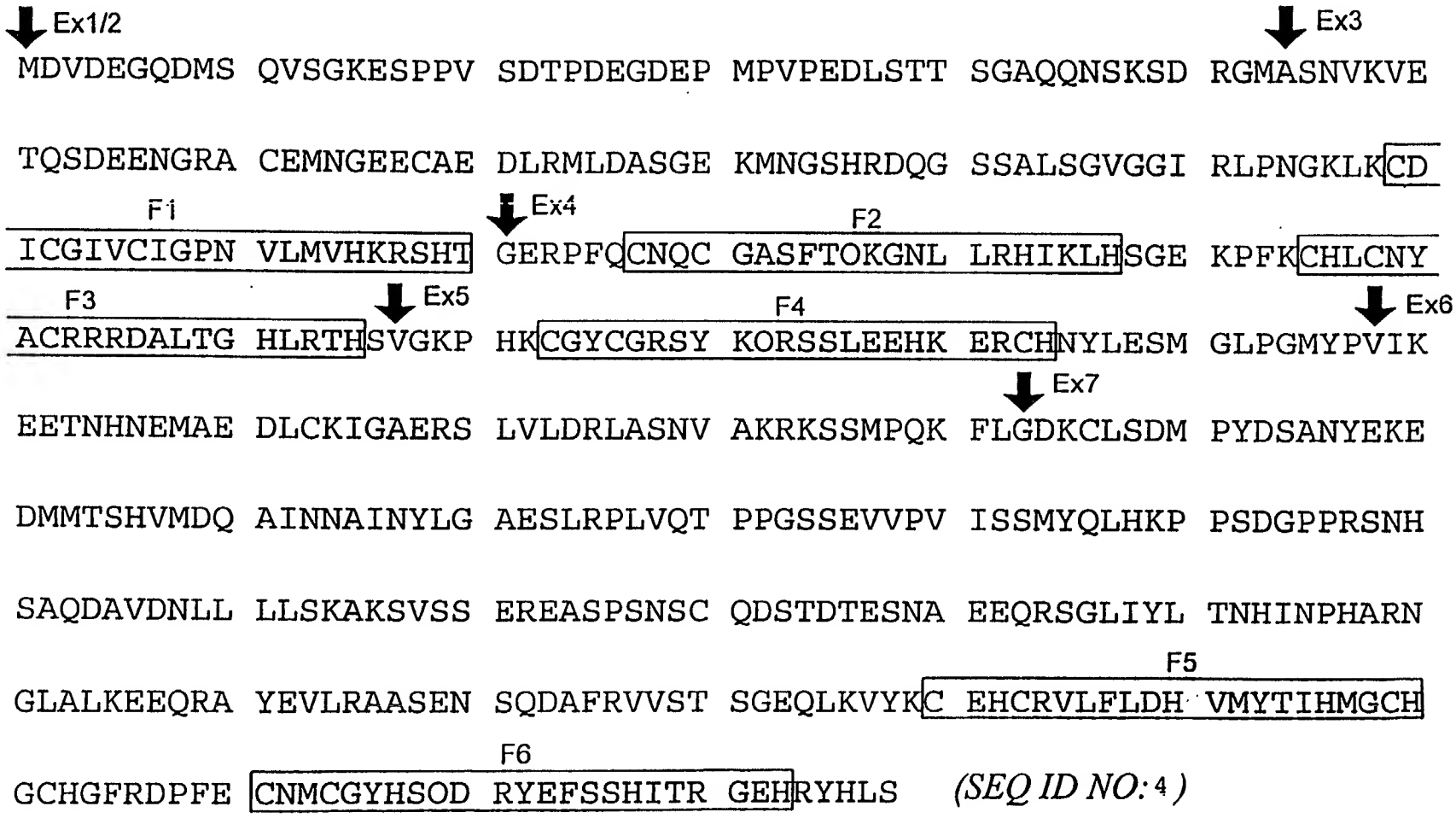
```
AAT GTT AAA GTA GAG ACT CAG AGT GAT GAA GAG AAT GGG CGT GCC TGT        48
Asn Val Lys Val Glu Thr Gln Ser Asp Glu Glu Asn Gly Arg Ala Cys
 1               5                  10                  15

GAA ATG AAT GGG GAA GAA TGT GCG GAG GAT TTA CGA ATG CTT GAT GCC        96
Glu Met Asn Gly Glu Glu Cys Ala Glu Asp Leu Arg Met Leu Asp Ala
            20                  25                  30

TCG GGA GAG AAA ATG AAT GGC TCC CAC AGG GAC CAA GGC AGC TCG GCT       144
Ser Gly Glu Lys Met Asn Gly Ser His Arg Asp Gln Gly Ser Ser Ala
        35                  40                  45

TTG TCG GGA GTT GGA GGC ATT CGA CTT CCT AAC GGA AAA CTA AAG TGT       192
Leu Ser Gly Val Gly Gly Ile Arg Leu Pro Asn Gly Lys Leu Lys Cys
    50                  55                  60

GAT ATC TGT GGG ATC ATT TGC ATC GGG CCC AAT GTG CTC ATG GTT CAC       240
Asp Ile Cys Gly Ile Ile Cys Ile Gly Pro Asn Val Leu Met Val His
65                  70                  75                  80

AAA AGA AGC CAC ACT GGA GAA CGG CCC TTC CAG TGC AAT CAG TGC GGG       288
Lys Arg Ser His Thr Gly Glu Arg Pro Phe Gln Cys Asn Gln Cys Gly
                85                  90                  95

GCC TCA TTC ACC CAG AAG GGC AAC CTG CTC CGG CAC ATC AAG CTG CAT       336
Ala Ser Phe Thr Gln Lys Gly Asn Leu Leu Arg His Ile Lys Leu His
            100                 105                 110

TCC GGG GAG AAG CCC TTC AAA TGC CAC CTC TGC AAC TAC GCC TGC CGC       384
Ser Gly Glu Lys Pro Phe Lys Cys His Leu Cys Asn Tyr Ala Cys Arg
        115                 120                 125

CGG AGG GAC GCC CTC ACT GGC CAC CTG AGG ACG CAC TCC GTT GGT AAA       432
Arg Arg Asp Ala Leu Thr Gly His Leu Arg Thr His Ser Val Gly Lys
    130                 135                 140

CCT CAC AAA TGT GGA TAT TGT GGC CGA AGC TAT AAA CAG CGA ACG TCT       480
Pro His Lys Cys Gly Tyr Cys Gly Arg Ser Tyr Lys Gln Arg Thr Ser
145                 150                 155                 160

TTA GAG GAA CAT AAA GAG CGC TGC CAC AAC TAC TTG GAA AGC ATG GGC       528
Leu Glu Glu His Lys Glu Arg Cys His Asn Tyr Leu Glu Ser Met Gly
                165                 170                 175

CTT CCG GGC ACA CTG TAC CCA GTC ATT AAA GAA GAA ACT AAG CAC AGT       576
Leu Pro Gly Thr Leu Tyr Pro Val Ile Lys Glu Glu Thr Lys His Ser
            180                 185                 190

GAA ATG GCA GAA GAC CTG TGC AAG ATA GGA TCA GAG AGA TCT CTC GTG       624
Glu Met Ala Glu Asp Leu Cys Lys Ile Gly Ser Glu Arg Ser Leu Val
        195                 200                 205

CTG GAC AGA CTA GCA AGT AAT GTC GCC AAA CGT AAG AGC TCT ATG CCT       672
Leu Asp Arg Leu Ala Ser Asn Val Ala Lys Arg Lys Ser Ser Met Pro
    210                 215                 220

CAG AAA TTT CTT GGG GAC AAG GGC CTG TCC GAC ACG CCC TAC GAC AGT       720
Gln Lys Phe Leu Gly Asp Lys Gly Leu Ser Asp Thr Pro Tyr Asp Ser
225                 230                 235                 240
```

FIG. 2A

```
GCC ACG TAC GAG AAG GAG AAC GAA ATG ATG AAG TCC CAC GTG ATG GAC      768
Ala Thr Tyr Glu Lys Glu Asn Glu Met Met Lys Ser His Val Met Asp
                245                 250                 255

CAA GCC ATC AAC AAC GCC ATC AAC TAC CTG GGG GCC GAG TCC CTG CGC      816
Gln Ala Ile Asn Asn Ala Ile Asn Tyr Leu Gly Ala Glu Ser Leu Arg
            260                 265                 270

CCG CTG GTG CAG ACG CCC CCG GGC GGT TCC GAG GTG GTC CCG GTC ATC      864
Pro Leu Val Gln Thr Pro Pro Gly Gly Ser Glu Val Val Pro Val Ile
        275                 280                 285

AGC CCG ATG TAC CAG CTG CAC AGG CGC TCG GAG GGC ACC CCG CGC TCC      912
Ser Pro Met Tyr Gln Leu His Arg Arg Ser Glu Gly Thr Pro Arg Ser
    290                 295                 300

AAC CAC TCG GCC CAG GAC AGC GCC GTG GAG TAC CTG CTG CTG CTC TCC      960
Asn His Ser Ala Gln Asp Ser Ala Val Glu Tyr Leu Leu Leu Leu Ser
305                 310                 315                 320

AAG GCC AAG TTG GTG CCC TCG GAG CGC GAG GCG TCC CCG AGC AAC AGC     1008
Lys Ala Lys Leu Val Pro Ser Glu Arg Glu Ala Ser Pro Ser Asn Ser
                325                 330                 335

TGC CAA GAC TCC ACG GAC ACC GAG AGC AAC AAC GAG GAG CAG CGC AGC     1056
Cys Gln Asp Ser Thr Asp Thr Glu Ser Asn Asn Glu Glu Gln Arg Ser
            340                 345                 350

GGT CTT ATC TAC CTG ACC AAC CAC ATC GCC CGA CGC GCG CAA CGC GTG     1104
Gly Leu Ile Tyr Leu Thr Asn His Ile Ala Arg Arg Ala Gln Arg Val
        355                 360                 365

TCG CTC AAG GAG GAG CAC CGC GCC TAC GAC CTG CTG CGC GCC GCC TCC     1152
Ser Leu Lys Glu Glu His Arg Ala Tyr Asp Leu Leu Arg Ala Ala Ser
    370                 375                 380

GAG AAC TCG CAG GAC GCG CTC CGC GTG GTC AGC ACC AGC GGG GAG CAG     1200
Glu Asn Ser Gln Asp Ala Leu Arg Val Val Ser Thr Ser Gly Glu Gln
385                 390                 395                 400

ATG AAG GTG TAC AAG TGC GAA CAC TGC CGG GTG CTC TTC CTG GAT CAC     1248
Met Lys Val Tyr Lys Cys Glu His Cys Arg Val Leu Phe Leu Asp His
                405                 410                 415

GTC ATG TAC ACC ATC CAC ATG GGC TGC CAC GGC TTC CGT GAT CCT TTT     1296
Val Met Tyr Thr Ile His Met Gly Cys His Gly Phe Arg Asp Pro Phe
            420                 425                 430

GAG TGC AAC ATG TGC GGC TAC CAC AGC CAG GAC CGG TAC GAG TTC TCG     1344
Glu Cys Asn Met Cys Gly Tyr His Ser Gln Asp Arg Tyr Glu Phe Ser
        435                 440                 445

TCG CAC ATA ACG CGA GGG GAG CAC CGC TTC CAC ATG AGC TAA             1386
Ser His Ile Thr Arg Gly Glu His Arg Phe His Met Ser
    450                 455                 460
```

(SEQ.ID.NO: 2)

FIG. 2B


Ex1/2
Ex3
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TQSDEENGRA CEMNGEECAE DLRMLDASGE KMNGSHRDQG SSALSGVGGI RLPNGKLKCD
F1
Ex4
F2
ICGIVCIGPN VLMVHKRSHT GERPFQCNQC GASFTOKGNL LRHIKLHSGE KPFKCHLCNY
F3
Ex5
F4
Ex6
ACRRRDALTG HLRTHSVGKP HKCGYCGRSY KORSSLEEHK ERCHNYLESM GLPGMYPVIK
Ex7
EETNHNEMAE DLCKIGAERS LVLDRLASNV AKRKSSMPQK FLGDKCLSDM PYDSANYEKE
DMMTSHVMDQ AINNAINYLG AESLRPLVQT PPGSSEVVPV ISSMYQLHKP PSDGPPRSNH
SAQDAVDNLL LLSKAKSVSS EREASPSNSC QDSTDTESNA EEQRSGLIYL TNHINPHARN
F5
GLALKEEQRA YEVLRAASEN SQDAFRVVST SGEQLKVYKC EHCRVLFLDH VMYTIHMGCH
F6
GCHGFRDPFE CNMCGYHSOD RYEFSSHITR GEHRYHLS (SEQ ID NO: 4)

FIG. 3

TOSOTO" DE8SSZ6D

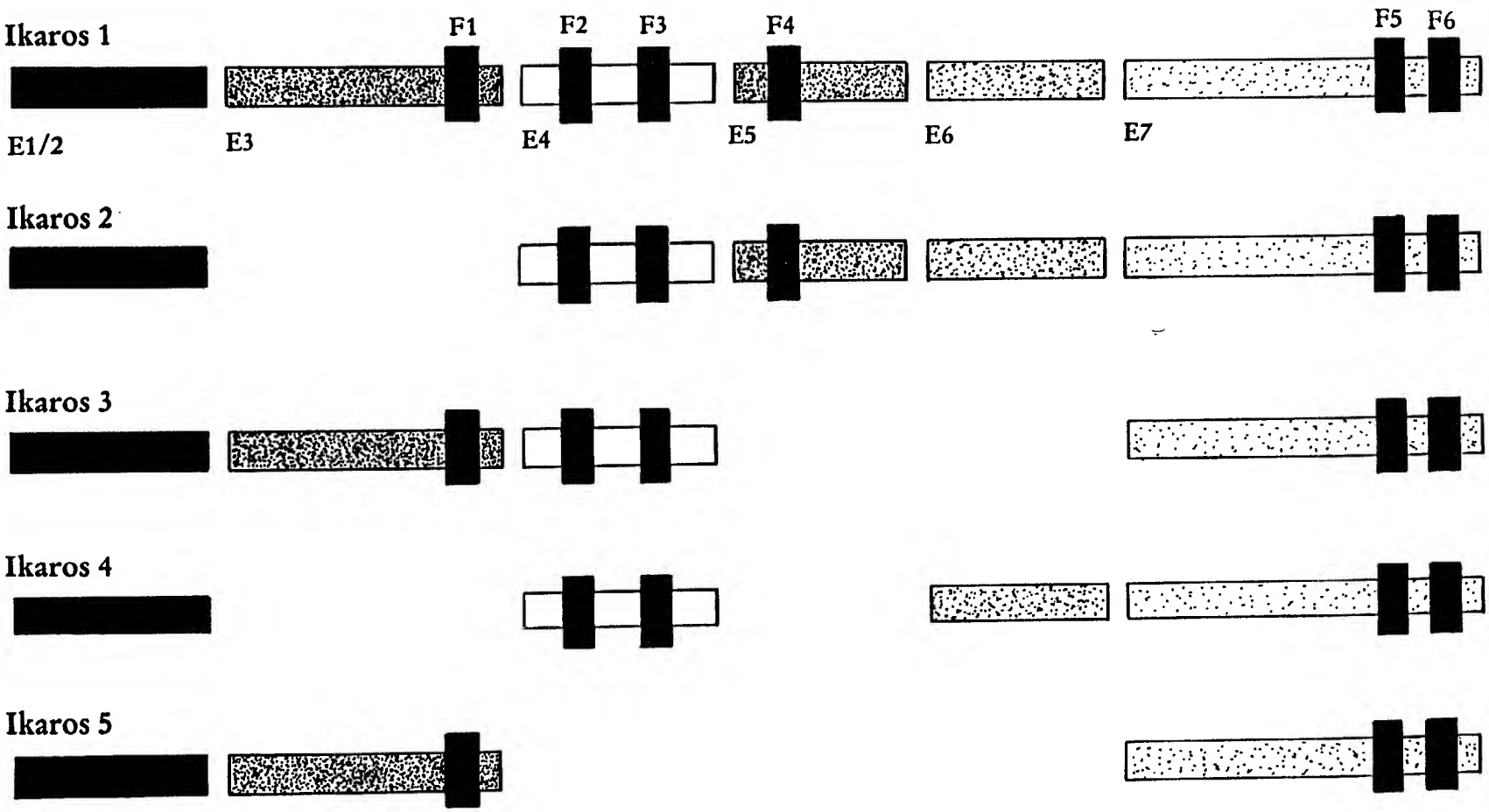
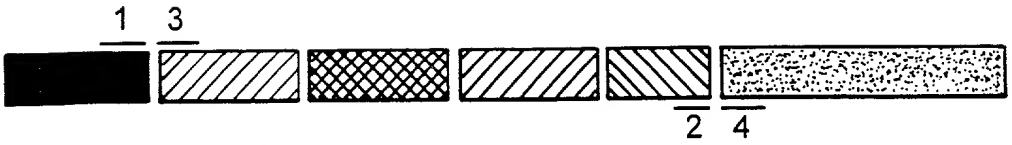


FIG. 4



Oligo1/2 IK-1/IK-2/IK-4

Oligo3/4 IK-1/IK-3/IK-5

FIG. 5

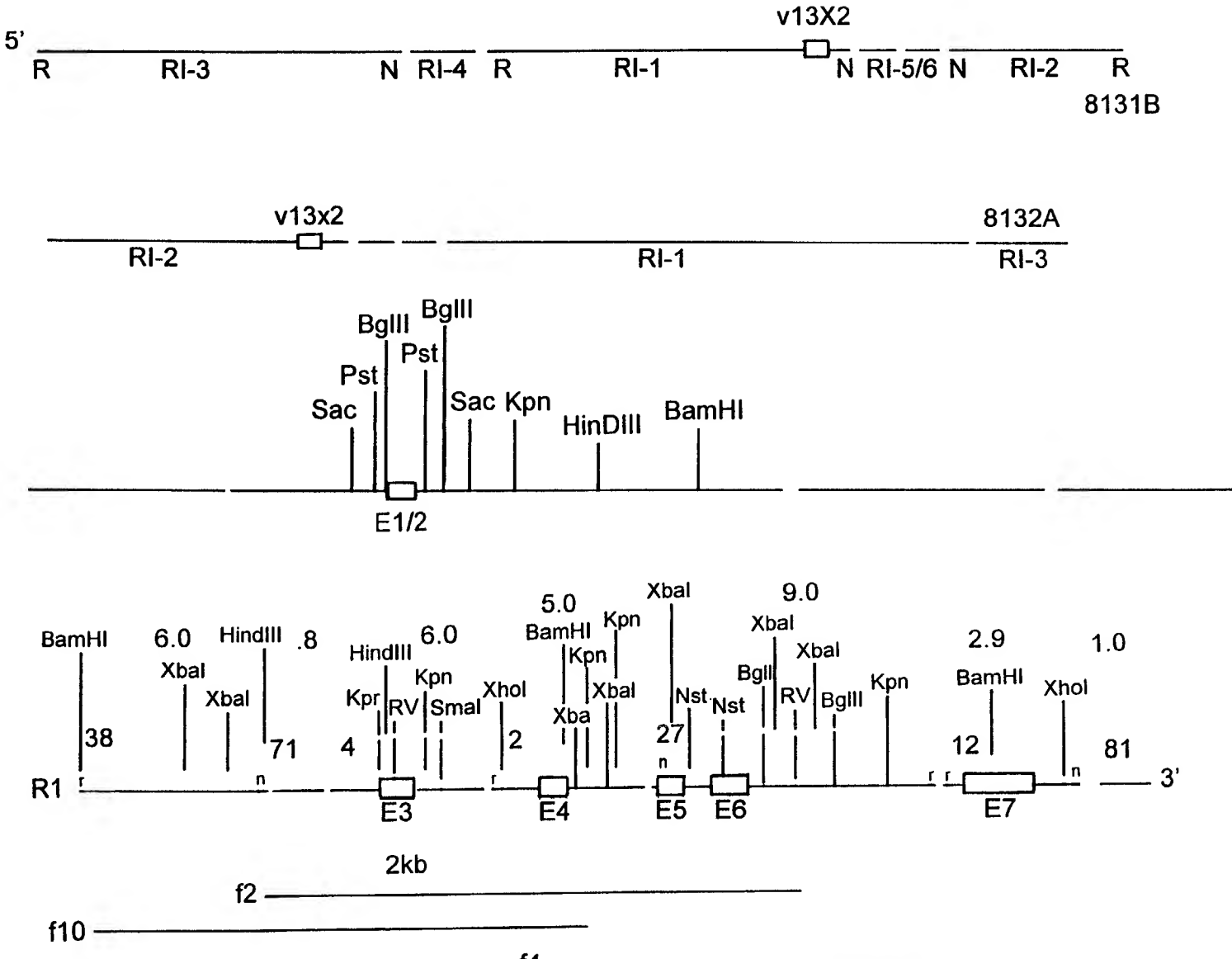

5'
v13X2
R
RI-3
N
RI-4
R
RI-1
N
RI-5/6
N
RI-2
R
8131B
v13x2
8132A
RI-2
RI-1
RI-3
BglII
BglII
Pst
Pst
Sac
Sac
Kpn
HinDIII
BamHI
E1/2
BamHI
6.0
HindIII
.8
XbaI
XbaI
38
71
HindIII
6.0
Kpr
RV
Kpn
SmaI
XhoI
4
2
5.0
BamHI
Kpn
Kpn
XbaI
Xba
XbaI
9.0
Nst
Nst
XbaI
XbaI
BglI
RV
BglII
Kpn
27
2.9
1.0
BamHI
XhoI
12
81
R1
3'
E3
E4
E5
E6
E7
2kb
f2
f10
f4
f8

FIG. 6

An Ikaros view of the hemopoletic system; expression and potential roles in development

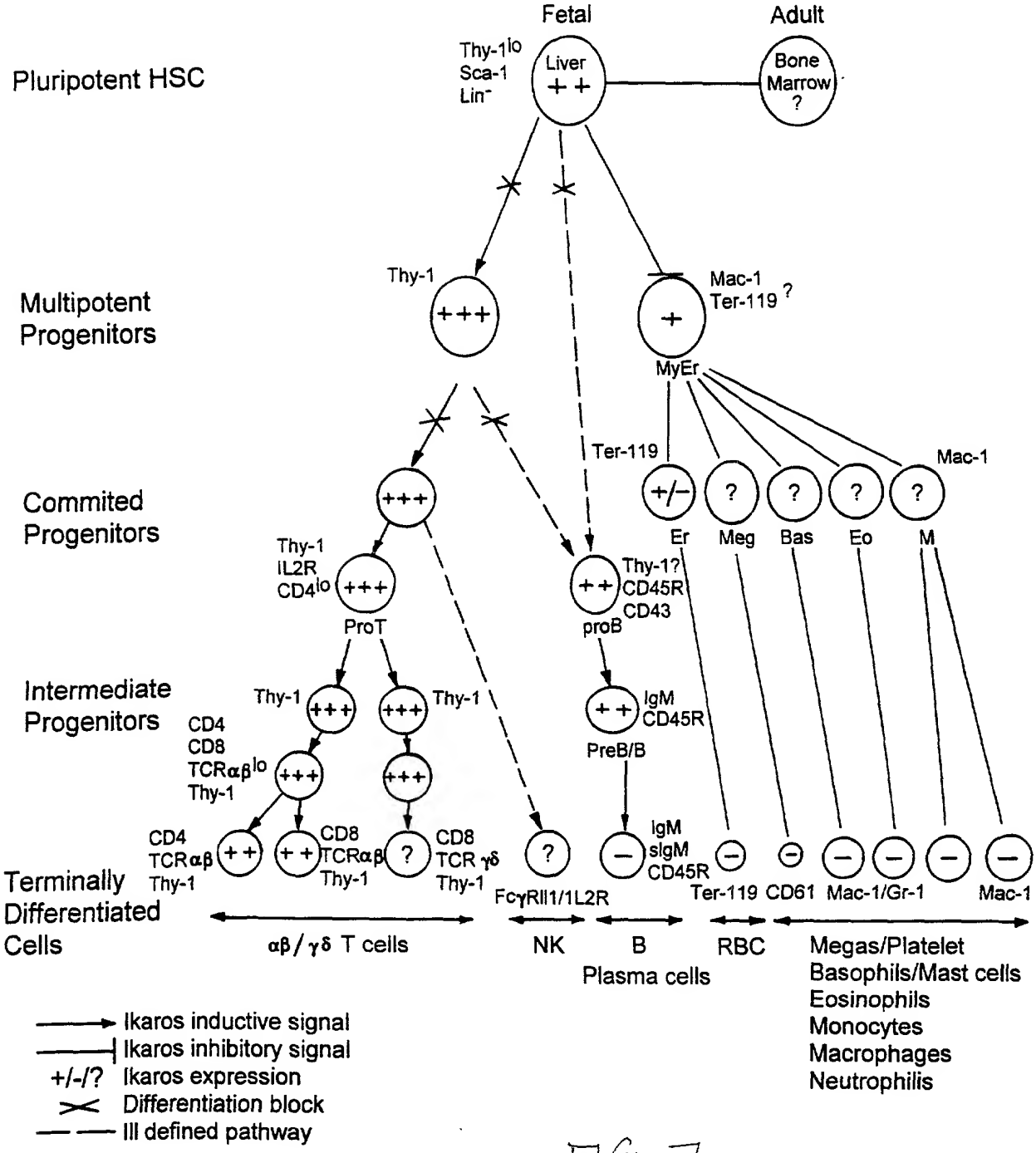
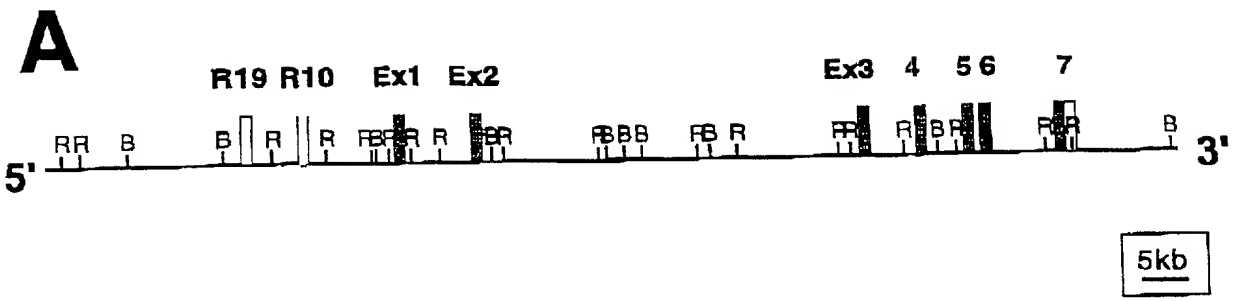


FIG. 7


A
R19 R10
Ex1
Ex2
Ex3
4
5 6
7
5'
3'
5kb

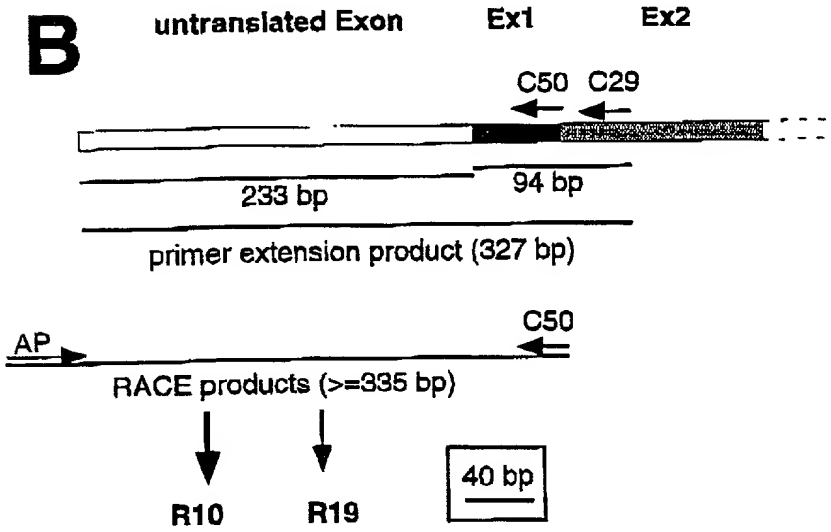

B
untranslated Exon
Ex1
Ex2
C50
C29
233 bp
94 bp
primer extension product (327 bp)
C50
AP
RACE products (>=335 bp)
R10
R19
40 bp

FIG. 8

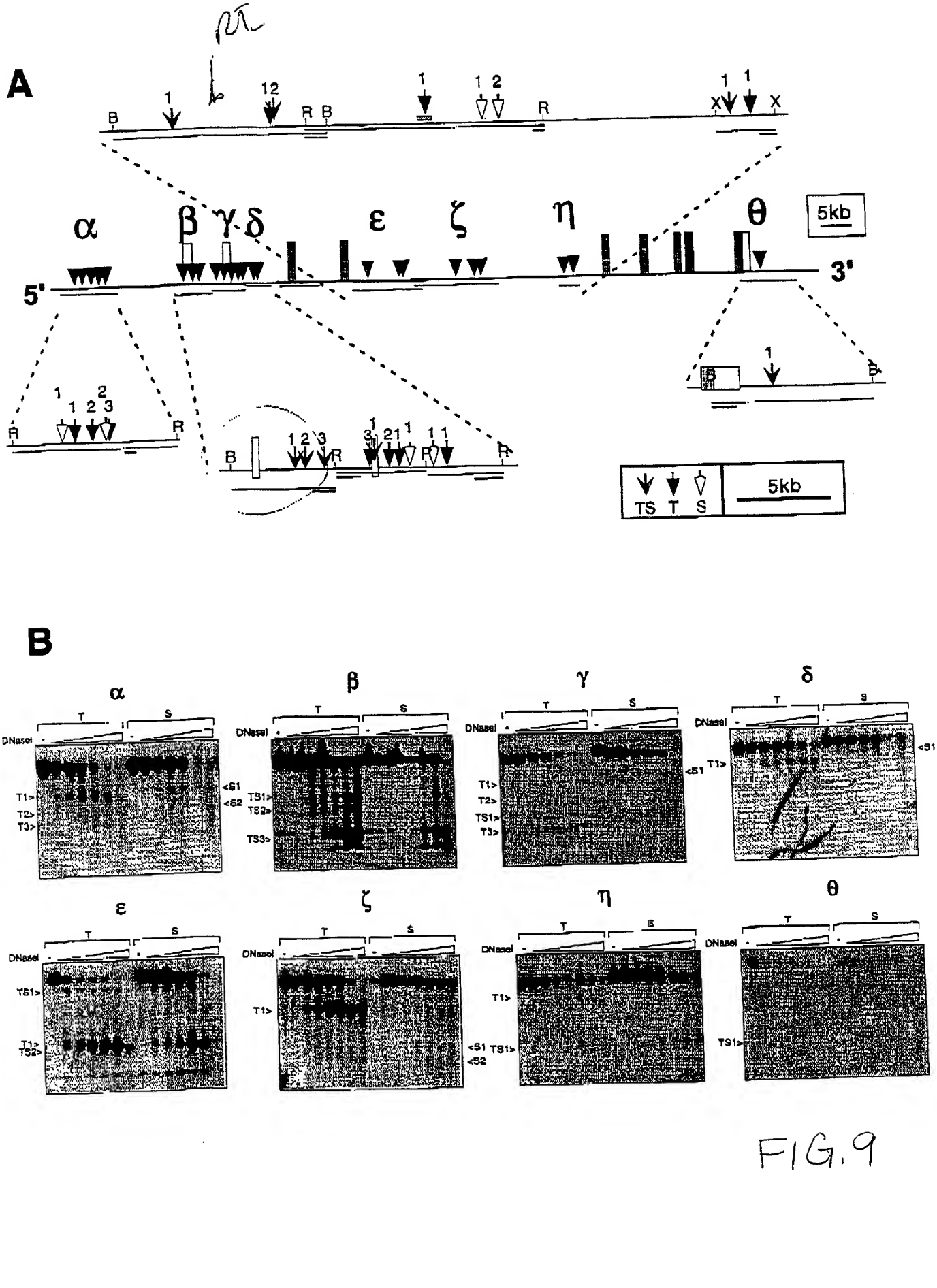
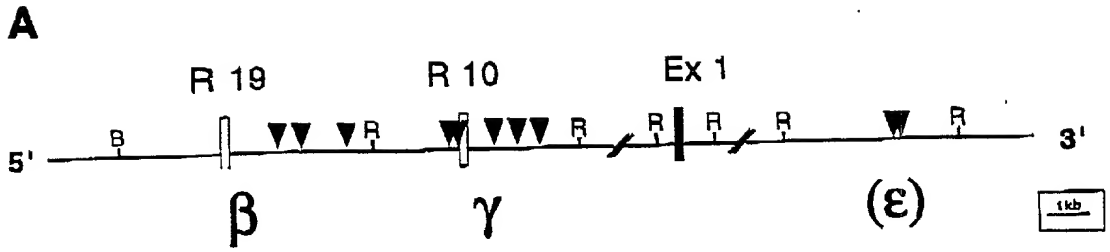


FIG. 9


A
R 19
R 10
Ex 1
5'
3'
B
R
β
γ
(ε)
1kb

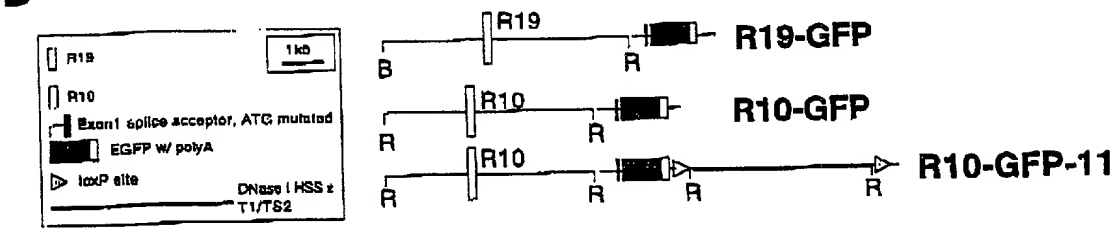
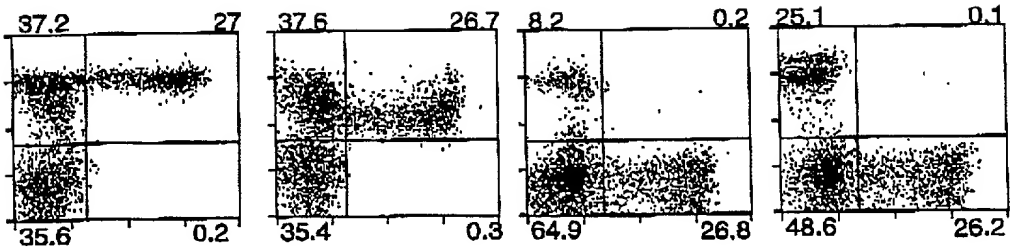

B
R19
R10
Exon1 splice acceptor, ATG mutated
EGFP w/ polyA
loxP site
DNase I HSS 2
T1/TS2
1kb
R19
R19-GFP
R10
R10-GFP
R10
R10-GFP-11
B
R

FIG. 10

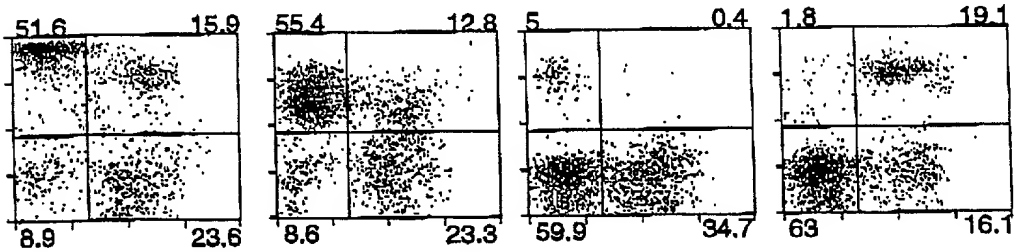
PCT/US99/05459

Bone Marrow

R19-GFP F



R10-GFP C



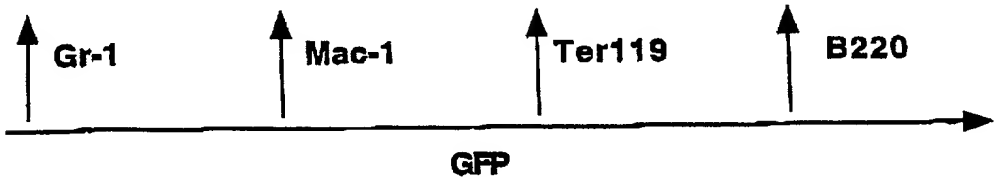
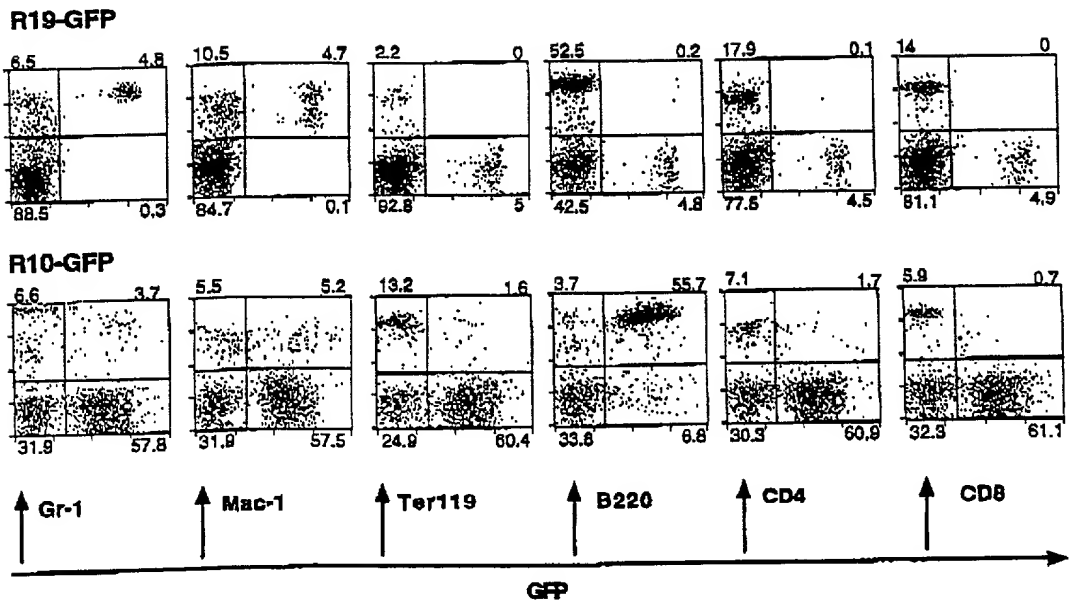


FIG. 11

Spleen



FIG, 12

SCANNED, # 18

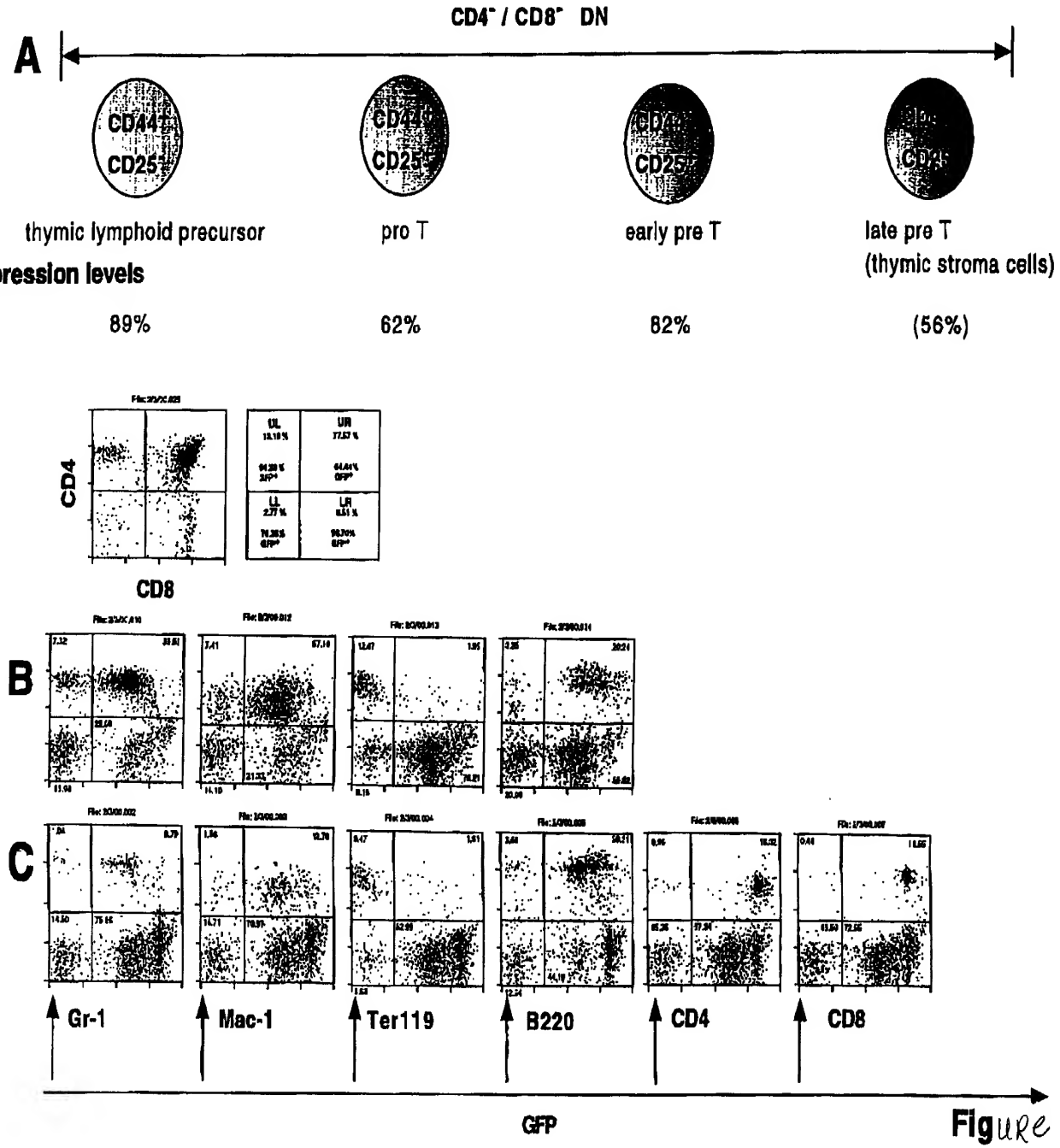


Figure 13